

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Holtzman, Douglas A. Group No.: 1652
 Application No.: 09/782,980
 Filed: February 13, 2001 Examiner: Maryam Monshipouri, Ph.D.
 For: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND STMST PROTEIN
 AND NUCLEIC ACID MOLECULES AND USES THEREFOR

Commissioner for Patents
 Washington, DC 20231

RESPONSE TO RESTRICTION REQUIREMENT

Dear Madam:

REMARKS

In response to the Restriction Requirement dated June 12, 2003 (Paper No. 11), Applicants hereby elect Group 9b, drawn to isolated DNA sequences encoding human STMST-2 polypeptides, host cells, kits comprising said sequences, and methods of expressing said sequences (claims 1-7, 12, 18, and 53-54), with traverse. This election is made without prejudice to Applicant's right to pursue the non-elected subject matter in other applications in the event a generic claim is not found allowable.

Applicants respectfully traverse the present restriction and reserve the right to petition therefrom under 37 C.F.R. § 1.144 and for the reasons set forth below.

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) AND 1.10*

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#12
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Elected as Separate Species of a Common Genus

Applicants submit that the separate nucleic acid sequences encoding SEQ ID NOs:71 and 74 (STMST-1 and STMST-2, respectively) should be examined together, as species of a common genus. As seen in the enclosed protein sequence alignment (Exhibit A), the sequences of SEQ ID NOs:71 and 74 (and the nucleic acid sequences encoding them) are related in that SEQ ID NO:74 (STMST-2), which is a 609 residue protein, comprises the majority portion of SEQ ID NO:71 (STMST-1), which is a 297 residue protein. Both protein sequences share the first 262 residues, which constitute over 88% of the entire length of the STMST-1 protein. The nucleic acid sequence encoding the protein sequences are even more similar, as evidenced by the enclosed alignment of the open reading frame encoding STMST-1 and a truncated version of the open reading frame encoding STMST-2 (Exhibit B, showing 93% sequence identity over the length of the STMST-1 open reading frame).

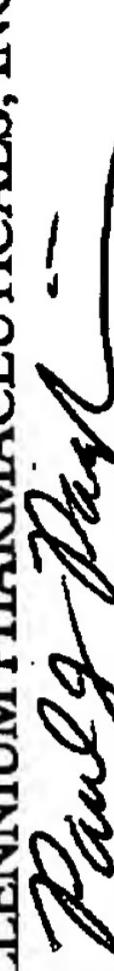
The inclusion of both nucleic acids which encode SEQ ID NOs:71 and 74 in the current election does not pose a serious examination burden on the Examiner. In fact, it would require virtually the same search and examination, since searching and examining nucleic acids that encode SEQ ID NO:74 includes by necessity a search and examination of the nucleic acids that encode SEQ ID NO:71 (SEQ ID NO:71 shares residues 1-262 of SEQ ID NO:74).

This paper is being filed timely, as it is believed that no extensions of time are required. In the event any extensions of time are deemed necessary, the undersigned hereby authorizes the requisite fees to be charged to Deposit Account No. 501668.

Entry of the remarks made herein is respectfully requested.

Respectfully submitted,

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July 14, 2003

```
>STMST1
>STMST2
scoring matrix: BLOSUM50, gap penalties: -12/-2
46.8% identity;
Global alignment score: 1198
--: --: 609 aa
```

scoring matrix: BLOSUM50, gap penalties: -12/-2
Global alignment score: 1198

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005

STMST1 --DCL---P
: :
STMST2 HSDSLGSAS

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```
-->stmmst1  
-->stmmst2 (truncated)  
scoring matrix: DNA, gap penalties: -16/-4  
93.0% identity; Global alignment score: 3863  
891 nt
```

truncated, matrix: DNA, gap penalties: -16/-4 identity: Global alignment score

penalties: -18/-4 Global alignment score: 3863

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610 620 630 640 650 660
/tmp/s GTGGAGGTGGGGCCAGGGCCACCAACCGGCCCTTCACCGTGCCCCACCATCGTGGTGGAG
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
stmt2 GTGGAGGTGGGGCCAGGGCCACCAACCGGCCCTTCACCGTGCCCCACCATCGTGGTGGAG
610 620 630 640 650 660
610 620 630 640 650 660
670 680 690 700 710 720
/tmp/s GACGGGCAGGGCAAGGGGCAAGGGGCTCCATCGATGGCTCGGAAGCCCCCAAACCTCTCTG
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
stmt2 GACGGGCAGGGCAAGGGCAAGGGCATTCCATCGATGGCTCGGAAGCCCCCAAACCTCTCTG
670 680 690 700 710 720
730 740 750 760 770 780
/tmp/s CAGACCACGGGCCCTCGTGAACCAATAGTCTTCATCGACTGCCTCATGGCTTCATGGCTTCCT
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
stmt2 CAGACCACGGGCCCTCGTGAACCAATAGTCTTCATCGACTGCCTCATGGCTTCATGGCTTCCT
730 740 750 760 770 780
790 800 810 820 830
/tmp/s GTGCTGGACTCTACGCCATCCCCGAAAGGTCTGCAGTGAGACAGGG-AGAGGACTGG--
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
stmt2 GTGCTGGTGGTGAACCTCAGGCC---CTGCGGGCCGACGGCTCAGGCCCTGGAT
790 800 810 820 830
840 850 860 870 880 890
/tmp/s GGCAAAAGAACCGAGCCTGAGGGTTTCAT---CCAAGGCAGGCCAAGAACCTGCC-C
::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
stmt2 GGCAACTCTGCCTGCTGTGGCTGGCTGGCCCTGCTGCCCTGCTGCCCTGCTGCCCT
840 850 860 870 880 890

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Practitioner's Docket No. MPI00-544OMNIM

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Submitted herewith:

Response to Restriction Requirement
Exhibit A
Exhibit B
Total

(2 pages)
(2 pages)
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(7 pages-including fax cover sheet)

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